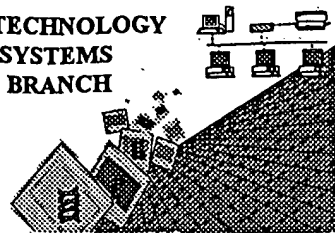


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



#17  
BC

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/937,665  
Source: PCT09  
Date Processed by STIC: 5/13/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

PC709

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/937,665

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓      Use of <220>      Sequence(s) 9-13 missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



**Does Not Comply**  
**Corrected Diskette Needed**

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/937,665

DATE: 03/13/2002 *Errors on pp. 4+5*  
TIME: 13:58:01

Input Set : A:\1825seq.txt  
Output Set: N:\CRF3\03132002\I937665.raw

3 <110> APPLICANT: Toni, Kutchan  
4       Anthony, Fist  
5       David, Atkins  
6       Meinhart, Zenk  
8 CODEINONE REDUCTASE FROM ALKALOID POPPY  
W--> 0 <120> TITLE INVENTION:  
10 <130> FILE REFERENCE: J&J-1825  
12 <140> CURRENT APPLICATION NUMBER: 09/937665  
C--> 13 <141> CURRENT FILING DATE: 2002-02-20  
15 <150> PRIOR APPLICATION NUMBER: PCT/AU00/00249  
16 <151> PRIOR FILING DATE: 2000-03-24  
18 <150> PRIOR APPLICATION NUMBER: AU PP 9463  
19 <151> PRIOR FILING DATE: 1999-03-26  
21 <160> NUMBER OF SEQ ID NOS: 25  
23 <170> SOFTWARE: PatentIn version 3.1  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 20  
27 <212> TYPE: DNA  
28 <213> ORGANISM: artificial sequence  
30 <220> FEATURE:  
31 <223> OTHER INFORMATION: PCR Primer  
33 <220> FEATURE:  
34 <221> NAME/KEY: misc\_feature  
35 <222> LOCATION: (3)..(3)  
36 <223> OTHER INFORMATION: n = A or G  
39 <220> FEATURE:  
40 <221> NAME/KEY: misc\_feature  
41 <222> LOCATION: (6)..(6)  
42 <223> OTHER INFORMATION: n = T or C  
45 <220> FEATURE:  
46 <221> NAME/KEY: misc\_feature  
47 <222> LOCATION: (9)..(9)  
48 <223> OTHER INFORMATION: n = T or C  
51 <220> FEATURE:  
52 <221> NAME/KEY: misc\_feature  
53 <222> LOCATION: (12)..(12)  
54 <223> OTHER INFORMATION: n = A or T or C  
57 <220> FEATURE:  
58 <221> NAME/KEY: misc\_feature  
59 <222> LOCATION: (15)..(15)  
60 <223> OTHER INFORMATION: n = T or G  
63 <220> FEATURE:  
64 <221> NAME/KEY: misc\_feature

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/937,665

DATE: 03/13/2002

TIME: 13:58:01

Input Set : A:\1825seq.txt

Output Set: N:\CRF3\03132002\I937665.raw

```

65 <222> LOCATION: (18)..(18)
66 <223> OTHER INFORMATION: n = T or C
69 <400> SEQUENCE: 1
W--> 70 gancntttna tnacntcnaa 20
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 26
75 <212> TYPE: DNA
76 <213> ORGANISM: artificial sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: PCR Primer
81 <220> FEATURE:
82 <221> NAME/KEY: misc_feature
83 <222> LOCATION: (3)..(3)
84 <223> OTHER INFORMATION: n = G or A
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <222> LOCATION: (15)..(15)
90 <223> OTHER INFORMATION: n = i
93 <220> FEATURE:
94 <221> NAME/KEY: misc_feature
95 <222> LOCATION: (21)..(21)
96 <223> OTHER INFORMATION: n = i
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (18)..(18)
102 <223> OTHER INFORMATION: n = T or A
105 <220> FEATURE:
106 <221> NAME/KEY: misc_feature
107 <222> LOCATION: (19)..(19)
108 <223> OTHER INFORMATION: n = T or G
111 <220> FEATURE:
112 <221> NAME/KEY: misc_feature
113 <222> LOCATION: (24)..(24)
114 <223> OTHER INFORMATION: n = T or C
117 <400> SEQUENCE: 2
W--> 118 gtngtctaac gtcancgnnc nccntt 26
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 21
123 <212> TYPE: DNA
124 <213> ORGANISM: artificial sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: PCR Primer
129 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
131 <222> LOCATION: (3)..(3)
132 <223> OTHER INFORMATION: n = i
135 <220> FEATURE:
136 <221> NAME/KEY: misc_feature
137 <222> LOCATION: (6)..(6)

```

## RAW SEQUENCE LISTING

DATE: 03/13/2002

PATENT APPLICATION: US/09/937,665

TIME: 13:58:01

Input Set : A:\1825seq.txt

Output Set: N:\CRF3\03132002\I937665.raw

```

138 <223> OTHER INFORMATION: n = c or g
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature
143 <222> LOCATION: (18)..(18)
144 <223> OTHER INFORMATION: n = t or c
147 <220> FEATURE:
148 <221> NAME/KEY: misc_feature
149 <222> LOCATION: (12)..(12)
150 <223> OTHER INFORMATION: n = t or c
153 <400> SEQUENCE: 3
W--> 154 cancanttag tncacctnta c 21
157 <210> SEQ ID NO: 4
158 <211> LENGTH: 29
159 <212> TYPE: DNA
160 <213> ORGANISM: artificial sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: PCR Primer
165 <220> FEATURE:
166 <221> NAME/KEY: misc_feature
167 <222> LOCATION: (6)..(6)
168 <223> OTHER INFORMATION: n = i
171 <220> FEATURE:
172 <221> NAME/KEY: misc_feature
173 <222> LOCATION: (9)..(9)
174 <223> OTHER INFORMATION: n = c or t
177 <220> FEATURE:
178 <221> NAME/KEY: misc_feature
179 <222> LOCATION: (12)..(12)
180 <223> OTHER INFORMATION: n = a or g
183 <220> FEATURE:
184 <221> NAME/KEY: misc_feature
185 <222> LOCATION: (18)..(18)
186 <223> OTHER INFORMATION: n = a or g
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (22)..(22)
192 <223> OTHER INFORMATION: n = a or t
195 <220> FEATURE:
196 <221> NAME/KEY: misc_feature
197 <222> LOCATION: (23)..(23)
198 <223> OTHER INFORMATION: n = g or c
201 <220> FEATURE:
202 <221> NAME/KEY: misc_feature
203 <222> LOCATION: (3)..(3)
204 <223> OTHER INFORMATION: n = i
207 <220> FEATURE:
208 <221> NAME/KEY: misc_feature
209 <222> LOCATION: (15)..(15)
210 <223> OTHER INFORMATION: n = i

```

## RAW SEQUENCE LISTING

DATE: 03/13/2002

PATENT APPLICATION: US/09/937,665

TIME: 13:58:01

Input Set : A:\1825seq.txt

Output Set: N:\CRF3\03132002\I937665.raw

213 <220> FEATURE:  
 214 <221> NAME/KEY: misc\_feature  
 215 <222> LOCATION: (24)..(24)  
 216 <223> OTHER INFORMATION: n = i  
 219 <220> FEATURE:  
 220 <221> NAME/KEY: misc\_feature  
 221 <222> LOCATION: (27)..(27)  
 222 <223> OTHER INFORMATION: n = i  
 225 <400> SEQUENCE: 4  
 W--> 226 gtngtanaanc angtnganat gnnnccnac 29  
 229 <210> SEQ ID NO: 5  
 230 <211> LENGTH: 21  
 231 <212> TYPE: DNA  
 232 <213> ORGANISM: artificial sequence  
 234 <220> FEATURE:  
 235 <223> OTHER INFORMATION: RT-PCR Primer  
 237 <400> SEQUENCE: 5  
 238 atggagagta atggtgtacc t 21  
 241 <210> SEQ ID NO: 6  
 242 <211> LENGTH: 21  
 243 <212> TYPE: DNA  
 244 <213> ORGANISM: artificial sequence  
 246 <220> FEATURE:  
 247 <223> OTHER INFORMATION: RT-PCR Primer  
 249 <400> SEQUENCE: 6  
 250 tctaccattc actcctgaca g 21  
 253 <210> SEQ ID NO: 7  
 254 <211> LENGTH: 33  
 255 <212> TYPE: DNA  
 256 <213> ORGANISM: artificial sequence  
 258 <220> FEATURE:  
 259 <223> OTHER INFORMATION: Primer  
 261 <400> SEQUENCE: 7  
 262 atggctagca tggagagtaa tgggtgtacct atg 33  
 265 <210> SEQ ID NO: 8  
 266 <211> LENGTH: 33  
 267 <212> TYPE: DNA  
 268 <213> ORGANISM: artificial sequence  
 270 <220> FEATURE:  
 271 <223> OTHER INFORMATION: Primer  
 273 <400> SEQUENCE: 8  
 274 ctctctcaaga ccctactctt cctacctagg gaa 33  
 277 <210> SEQ ID NO: 9  
 278 <211> LENGTH: 7  
 279 <212> TYPE: PRT  
 280 <213> ORGANISM: artificial sequence  
 282 <220> FEATURE:  
 283 <223> OTHER INFORMATION: peptide  
 285 <220> FEATURE:

invalid response; must give genetic source.  
 See error summary sheet, item 11

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/937,665

DATE: 03/13/2002  
TIME: 13:58:01

Input Set : A:\1825seq.txt  
Output Set: N:\CRF3\03132002\I937665.raw

286 <221> NAME/KEY: MISC\_FEATURE  
287 <222> LOCATION: (1)..(1)  
288 <223> OTHER INFORMATION: x = any amino acid  
291 <400> SEQUENCE: 9  
W--> 293 Xaa Leu Gln Glu Leu Met Ala  
294 1 5  
297 <210> SEQ ID NO: 10  
298 <211> LENGTH: 11  
299 <212> TYPE: PRT  
300 <213> ORGANISM: artificial sequence  
302 <220> FEATURE:  
303 <223> OTHER INFORMATION: peptide *Some error*  
305 <400> SEQUENCE: 10  
307 Val Leu His Gln Ile Ala Val Ala Arg Gly Lys  
308 1 5 10  
311 <210> SEQ ID NO: 11  
312 <211> LENGTH: 10  
313 <212> TYPE: PRT  
314 <213> ORGANISM: artificial sequence  
316 <220> FEATURE:  
317 <223> OTHER INFORMATION: peptide *Some error*  
319 <400> SEQUENCE: 11  
321 Asp Asp Asp Glu Leu Phe Ile Thr Ser Lys  
322 1 5 10  
325 <210> SEQ ID NO: 12  
326 <211> LENGTH: 16  
327 <212> TYPE: PRT  
328 <213> ORGANISM: artificial sequence  
330 <220> FEATURE:  
331 <223> OTHER INFORMATION: peptide *Some error*  
333 <400> SEQUENCE: 12  
335 Ile Pro Asp Val Val Asn Gln Val Glu Met Ser Pro Thr Leu Gly Gln  
336 1 5 10 15  
339 <210> SEQ ID NO: 13  
340 <211> LENGTH: 7  
341 <212> TYPE: PRT  
342 <213> ORGANISM: artificial sequence  
344 <220> FEATURE:  
345 <223> OTHER INFORMATION: peptide *Some error*  
347 <220> FEATURE:  
348 <221> NAME/KEY: MISC\_FEATURE  
349 <222> LOCATION: (1)..(1)  
350 <223> OTHER INFORMATION: x = any amino acid  
353 <400> SEQUENCE: 13  
W--> 355 Xaa Val Asn Glu Ile Pro Lys  
356 1 5  
359 <210> SEQ ID NO: 14  
360 <211> LENGTH: 5  
361 <212> TYPE: PRT

## VERIFICATION SUMMARY

DATE: 03/13/2002

PATENT APPLICATION: US/09/937,665

TIME: 13:58:02

Input Set : A:\1825seq.txt

Output Set: N:\CRF3\03132002\I937665.raw

L:0 M:201 W: Mandatory field data missing, TITLE INVENTION  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15